

- 31 -

## SEQUENCE LISTING

## (I) GENERAL INFORMATION:

- (i) APPLICANT: (US ONLY): S. CORY, J.A. ADAMS, C. PRINT, L. GIBSON  
(OTHER THAN US) THE WALTER AND ELIZA HALL INSTITUTE  
OF MEDICAL RESEARCH
- (ii) TITLE OF INVENTION: A METHOD OF TREATMENT AND AN ANIMAL  
MODEL USEFUL FOR SAME
- (iii) NUMBER OF SEQUENCES: 8
- (iv) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE: DAVIES COLLISON CAVE  
(B) STREET: 1 LITTLE COLLINS STREET  
(C) CITY: MELBOURNE  
(D) STATE: VICTORIA  
(E) COUNTRY: AUSTRALIA  
(F) ZIP: 3000
- (v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER: PCT INTERNATIONAL  
(B) FILING DATE: 16-SEP-1998
- (vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: PO9228  
(B) FILING DATE: 16-SEP-1997
- (viii) ATTORNEY/AGENT INFORMATION:  
(A) NAME: HUGHES, DR E JOHN L  
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(C) TELEX: AA 31787

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a1

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- 32 -

## (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 582 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS  
 (B) LOCATION: 1..582

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATG GCG ACC CCA GCC TCG GCC CCA GAC ACA CGG GCT CTG GTG GCA GAC 48  
 Met Ala Thr Pro Ala Ser Ala Pro Asp Thr Arg Ala Leu Val Ala Asp  
 1 5 10 15

TTT GTA GGT TAT AAG CTG AGG CAG AAG GGT TAT GTC TGT GGA GCT GGC 96  
 Phe Val Gly Tyr Lys Leu Arg Gln Lys Gly Tyr Val Cys Gly Ala Gly  
 20 25 30

CCC GGG GAG GGC CCA GCA GCT GAC CCG CTG CAC CAA GCC ATG CGG GCA 144  
 Pro Gly Glu Gly Pro Ala Ala Asp Pro Leu His Gln Ala Met Arg Ala  
 35 40 45

GCT GGA GAT GAG TTC GAG ACC CGC TTC CGG CGC ACC TTC TCT GAT CTG 192  
 Ala Gly Asp Glu Phe Glu Thr Arg Phe Arg Arg Thr Phe Ser Asp Leu  
 50 55 60

GCG GCT CAG CTG CAT GTG ACC CCA GGC TCA GCC CAA CAA CGC TTC ACC 240  
 Ala Ala Gln Leu His Val Thr Pro Gly Ser Ala Gln Gln Arg Phe Thr  
 65 70 75 80

CAG GTC TCC GAT GAA CTT TTT CAA GGG GGC CCC AAC TGG GGC CGC CTT 288  
 Gln Val Ser Asp Glu Leu Phe Gln Gly Pro Asn Trp Gly Arg Leu  
 85 90 95

GTA GCC TTC TTT GTC TTT GGG GCT GCA CTG TGT GCT GAG AGT GTC AAC 336  
 Val Ala Phe Phe Val Phe Gly Ala Leu Cys Ala Glu Ser Val Asn  
 100 105 110

AAG GAG ATG GAA CCA CTG GTG GGA CAA GTG CAG GAG TGG ATG GTG GCC 384  
 Lys Glu Met Glu Pro Leu Val Gly Gln Val Gln Glu Trp Met Val Ala  
 115 120 125

TAC CTG GAG ACG CGG CTG GCT GAC TGG ATC CAC AGC AGT GGG GGC TGG 432  
 Tyr Leu Glu Thr Arg Leu Ala Asp Trp Ile His Ser Ser Gly Gly Trp  
 130 135 140

GCG GAG TTC ACA GCT CTA TAC GGG GAC GGG GCC CTG GAG GAG GCG CGG 480  
 Ala Glu Phe Thr Ala Leu Tyr Gly Asp Gly Ala Leu Glu Glu Ala Arg  
 145 150 155 160

CGT CTG CGG GAG GGG AAC TGG GCA TCA GTG AGG ACA GTG CTG ACG GGG 528  
 Arg Leu Arg Glu Gly Asn Trp Ala Ser Val Arg Thr Val Leu Thr Gly  
 165 170 175

GCC GTG GCA CTG GGG GCC CTG GTA ACT GTA GGG GCC TTT TTT GCT AGC 576  
 Ala Val Ala Leu Gly Ala Leu Val Thr Val Gly Ala Phe Phe Ala Ser  
 180 185 190

AAG TG 582  
 Lys

00508745-07100

- 33 -

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ala Thr Pro Ala Ser Ala Pro Asp Thr Arg Ala Leu Val Ala Asp  
1 5 10 15  
Phe Val Gly Tyr Lys Leu Arg Gln Lys Gly Tyr Val Cys Gly Ala Gly  
20 25 30  
Pro Gly Glu Gly Pro Ala Ala Asp Pro Leu His Gln Ala Met Arg Ala  
35 40 45  
Ala Gly Asp Glu Phe Glu Thr Arg Phe Arg Arg Thr Phe Ser Asp Leu  
50 55 60  
Ala Ala Gln Leu His Val Thr Pro Gly Ser Ala Gln Gln Arg Phe Thr  
65 70 75 80  
Gln Val Ser Asp Glu Leu Phe Gln Gly Gly Pro Asn Trp Gly Arg Leu  
85 90 95  
Val Ala Phe Phe Val Phe Gly Ala Ala Leu Cys Ala Glu Ser Val Asn  
100 105 110  
Lys Glu Met Glu Pro Leu Val Gly Gln Val Gln Glu Trp Met Val Ala  
115 120 125  
Tyr Leu Glu Thr Arg Leu Ala Asp Trp Ile His Ser Ser Gly Gly Trp  
130 135 140  
Ala Glu Phe Thr Ala Leu Tyr Gly Asp Gly Ala Leu Glu Glu Ala Arg  
145 150 155 160  
Arg Leu Arg Glu Gly Asn Trp Ala Ser Val Arg Thr Val Leu Thr Gly  
165 170 175  
Ala Val Ala Leu Gly Ala Leu Val Thr Val Gly Ala Phe Phe Ala Ser  
180 185 190  
Lys

00500745-071200

- 34 -

## (2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 582 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

- (ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 1..582

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATG GCG ACC CCA GCC TCA ACC CCA GAC ACA CGG GCT CTA GTG GCT GAC	49
Met Ala Thr Pro Ala Ser Thr Pro Asp Thr Arg Ala Leu Val Ala Asp	
1 5 10 15	
TTT GTA GGC TAT AAG CTG AGG CAG AAG GGT TAT GTC TGT GGA GCT GGC	96
Phe Val Gly Tyr Lys Leu Arg Gln Lys Gly Tyr Val Cys Gly Ala Gly	
20 25 30	
CCT GGG GAA GGC CCA GCC GCC GAC CCG CTG CAC CAA GCC ATG CGG GCT	144
Pro Gly Glu Gly Pro Ala Ala Asp Pro Leu His Gln Ala Met Arg Ala	
35 40 45	
GCT GGA GAC GAG TTT GAG ACC CGT TTC CGC CGC ACC TTC TCT GAC CTG	192
Ala Gly Asp Glu Phe Glu Thr Arg Phe Arg Arg Thr Phe Ser Asp Leu	
50 55 60	
GCC GCT CAG CTA CAC GTG ACC CCA GGC TCA GCC CAG CAA CGC TTC ACC	240
Ala Ala Gln Leu His Val Thr Pro Gly Ser Ala Gln Gln Arg Phe Thr	
65 70 75 80	
CAG GTT TCC GAC GAA CTT TTC CAA GGG GGC CCT AAC TGG GGC CGT CTT	288
Gln Val Ser Asp Glu Leu Phe Gln Gly Gly Pro Asn Trp Gly Arg Leu	
85 90 95	
GTG GCA TTC TTT GTC TTT GGG GCT GCC CTG TGT GCT GAG AGT GTC AAC	336
Val Ala Phe Phe Val Phe Gly Ala Ala Leu Cys Ala Glu Ser Val Asn	
100 105 110	
AAA GAA ATG GAG CCT TTG GTG GGA CAA GTG CAG GAT TGG ATG GTG GCC	384
Lys Glu Met Glu Pro Leu Val Gly Gln Val Gln Asp Trp Met Val Ala	
115 120 125	
TAC CTG GAG ACA CGT CTG GCT GAC TGG ATC CAC AGC AGT GGG GGC TGG	432
Tyr Leu Glu Thr Arg Leu Ala Asp Trp Ile His Ser Ser Gly Gly Trp	
130 135 140	
GCG GAG TTC ACA GCT CTA TAC GGG GAC GGG GCC CTG GAG GAG GCA CGG	480
Ala Glu Phe Thr Ala Leu Tyr Gly Asp Gly Ala Leu Glu Glu Ala Arg	
145 150 155 160	
CGT CTG CGG GAG GGG AAC TGG GCA TCA GTG AGG ACA GTG CTG ACG GGG	528
Arg Leu Arg Glu Gly Asn Trp Ala Ser Val Arg Thr Val Leu Thr Gly	
165 170 175	
GCC GTG GCA CTG GGG GCC CTG GTA ACT GTA GGG GCC TTT TTT GCT AGC	576
Ala Val Ala Leu Gly Ala Leu Val Thr Val Gly Ala Phe Phe Ala Ser	
180 185 190	
AAG TG	582
Lys	

00506745-074200

- 35 -

## (2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 193 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Ala Thr Pro Ala Ser Thr Pro Asp Thr Arg Ala Leu Val Ala Asp  
 1 5 10 15  
 Phe Val Gly Tyr Lys Leu Arg Gln Lys Gly Tyr Val Cys Gly Ala Gly  
 20 25 30  
 Pro Gly Glu Gly Pro Ala Ala Asp Pro Leu His Gln Ala Met Arg Ala  
 35 40 45  
 Ala Gly Asp Glu Phe Glu Thr Arg Phe Arg Arg Thr Phe Ser Asp Leu  
 50 55 60  
 Ala Ala Gln Leu His Val Thr Pro Gly Ser Ala Gln Gln Arg Phe Thr  
 65 70 75 80  
 Gln Val Ser Asp Glu Leu Phe Gln Gly Gly Pro Asn Trp Gly Arg Leu  
 85 90 95  
 Val Ala Phe Phe Val Phe Gly Ala Ala Leu Cys Ala Glu Ser Val Asn  
 100 105 110  
 Lys Glu Met Glu Pro Leu Val Gly Gln Val Gln Asp Trp Met Val Ala  
 115 120 125  
 Tyr Leu Glu Thr Arg Leu Ala Asp Trp Ile His Ser Ser Gly Gly Trp  
 130 135 140  
 Ala Glu Phe Thr Ala Leu Tyr Gly Asp Gly Ala Leu Glu Glu Ala Arg  
 145 150 155 160  
 Arg Leu Arg Glu Gly Asn Trp Ala Ser Val Arg Thr Val Leu Thr Gly  
 165 170 175  
 Ala Val Ala Leu Gly Ala Leu Val Thr Val Gly Ala Phe Phe Ala Ser  
 180 185 190

Lys

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- 36 -

## (2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 583 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

- (ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 1..583

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATG GCG ACC CCA GCC TCG GCC CCA GAC ACA CGG GCT CTG GTG GCA GAC	48
Met Ala Thr Pro Ala Ser Ala Pro Asp Thr Arg Ala Leu Val Ala Asp	
1 5 10 15	
TTT GTA GGT TAT AAG CTG AGG CAG AAG GGT TAT GTC TGT GGA GCT GGC	96
Phe Val Gly Tyr Lys Leu Arg Gln Lys Gly Tyr Val Cys Gly Ala Gly	
20 25 30	
CCC GGG GAG GGC CCA GCA GCT GAC CCG CTG CAC CAA GCC ATG CGG GCA	144
Pro Gly Glu Gly Pro Ala Ala Asp Pro Leu His Gln Ala Met Arg Ala	
35 40 45	
GCT GGA GAT CAG TTC GAG ACC CGC TTC CGG CGC ACC TTC TCT GAT CTG	192
Ala Gly Asp Glu Phe Glu Thr Arg Phe Arg Arg Thr Phe Ser Asp Leu	
50 55 60	
GCG GCT CAG CTG CAT GTG ACC CCA GGC TCA GCC CAG CAA CGC TTC ACC	240
Ala Ala Gln Leu His Val Thr Pro Gly Ser Ala Gln Gln Arg Phe Thr	
65 70 75 80	
CAG GTC TCC GAC GAA CTT TTT CAA GGG GGC CCC AAC TGG GGC CGC CTT	288
Gln Val Ser Asp Glu Leu Phe Gln Gly Gly Pro Asn Trp Gly Arg Leu	
85 90 95	
GTA GCC TTC TTT CTC TTT GGG GCT GCA CTG TGT GCT GAG AGT GTC AAC	336
Val Ala Phe Phe Leu Phe Gly Ala Leu Cys Ala Glu Ser Val Asn	
100 105 110	
AAG GAG ATG GAA CCA CTG GTG GGA CAA GTG CAG GAG TGG ATG GTG GCC	384
Lys Glu Met Glu Pro Leu Val Gly Gln Val Gln Glu Trp Met Val Ala	
115 120 125	
TAC CTG GAG ACG CGG CTG GTC GAC TGG ATC CAC AGC AGT GGG GGC TGG	432
Tyr Leu Glu Thr Arg Leu Val Asp Trp Ile His Ser Ser Gly Gly Trp	
130 135 140	
GCG GAG TTC ACA GCT CTA TAC GGG GAC GGG GCC CTG GAG GAG GCG CGG	480
Ala Glu Phe Thr Ala Leu Tyr Gly Asp Gly Ala Leu Glu Glu Ala Arg	
145 150 155 160	
CGT CTG CGG GAG GGG AAC TGG GCA TCA GTG AGG ACA GTG CTG ACG GGG	528
Arg Leu Arg Glu Gly Asn Trp Ala Ser Val Arg Thr Val Leu Thr Gly	
165 170 175	
GCC GTG GCA CTG GGG GCC CTG GTA ACT GTA GGG GCC TTT TTT GCT AGC	576
Ala Val Ala Leu Gly Ala Leu Val Thr Val Gly Ala Phe Phe Ala Ser	
180 185 190	
AAG TGA A	583
Lys *	

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(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 194 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Ala Thr Pro Ala Ser Ala Pro Asp Thr Arg Ala Leu Val Ala Asp  
1 5 10 15

Phe Val Gly Tyr Lys Leu Arg Gln Lys Gly Tyr Val Cys Gly Ala Gly  
20 25 30

Pro Gly Glu Gly Pro Ala Ala Asp Pro Leu His Gln Ala Met Arg Ala  
35 40 45

Ala Gly Asp Glu Phe Glu Thr Arg Phe Arg Arg Thr Phe Ser Asp Leu  
50 55 60

Ala Ala Gln Leu His Val Thr Pro Gly Ser Ala Gln Gln Arg Phe Thr  
65 70 75 80

Gln Val Ser Asp Glu Leu Phe Gln Gly Gly Pro Asn Trp Gly Arg Leu  
85 90 95

Val Ala Phe Phe Leu Phe Gly Ala Ala Leu Cys Ala Glu Ser Val Asn  
100 105 110

Lys Glu Met Glu Pro Leu Val Gly Gln Val Gln Glu Trp Met Val Ala  
115 120 125

Tyr Leu Glu Thr Arg Leu Val Asp Trp Ile His Ser Ser Gly Gly Trp  
130 135 140

Ala Glu Phe Thr Ala Leu Tyr Gly Asp Gly Ala Leu Glu Glu Ala Arg  
145 150 155 160

Arg Leu Arg Glu Gly Asn Trp Ala Ser Val Arg Thr Val Leu Thr Gly  
165 170 175

Ala Val Ala Leu Gly Ala Leu Val Thr Val Gly Ala Phe Phe Ala Ser  
180 185 190

Lys \*

- 38 -

## (2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 582 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

- (ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 1..582

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATG CCG ACC CCA GCC TCA ACC CCA GAC ACA CGC GCT CTA GTG GCT GAC	48
Met Pro Thr Pro Ala Ser Thr Pro Asp Thr Arg Ala Leu Val Ala Asp	
1 5 10 15	
TTT GTA GGC TAT AGG CTG AGG CAG AAG GGT TAT GTC TGT GGA GCT GGG	96
Phe Val Gly Tyr Arg Leu Arg Gln Lys Gly Tyr Val Cys Gly Ala Gly	
20 25 30	
CCT GGG GAA GGC CCA GCC GCC GAC CCG CTG CAC CAA GCC ATG CGG GCT	144
Pro Gly Glu Gly Pro Ala Ala Asp Pro Leu His Gln Ala Met Arg Ala	
35 40 45	
GCT GGA GAC GAG TTT GAG ACC CGT TTC CGC CGC ACC TTC TCT GAC CTG	192
Ala Gly Asp Glu Phe Glu Thr Arg Phe Arg Arg Thr Phe Ser Asp Leu	
50 55 60	
GCC GCT CAG CTA CAC GTG ACC CCA GGC TCA GCC CAG CAA CGC TTC ACC	240
Ala Ala Gln Leu His Val Thr Pro Gly Ser Ala Gln Gln Arg Phe Thr	
65 70 75 80	
CAG GTT TCC GAC GAA CTT TTC CAA GGG GGC CCT AAC TGG GGC CGT CTT	288
Gln Val Ser Asp Glu Leu Phe Gln Gly Gly Pro Asn Trp Gly Arg Leu	
85 90 95	
GTG GCA TTC TTT GTC TTT GGG GCT GCC CTG TGT GCT GAG AGT GTC AAC	336
Val Ala Phe Phe Val Phe Gly Ala Ala Leu Cys Ala Glu Ser Val Asn	
100 105 110	
AAA GAA ATG GAG CCT TTG GTG GGA CAA GTC CAG GAT TGG ATC GTG GCC	384
Lys Glu Met Glu Pro Leu Val Gly Gln Val Gln Asp Trp Ile Val Ala	
115 120 125	
TAC CTG GAG ACA CGT CTG GCT GAC TGG ATC CAC AGC AGT GGC GGC TGG	432
Tyr Leu Glu Thr Arg Leu Ala Asp Trp Ile His Ser Ser Gly Gly Trp	
130 135 140	
GCG GAC TTC ACA GCT CTA TAC GGG GAC GGG GCC CTG GAG GAC GCA CGG	480
Ala Asp Phe Thr Ala Leu Tyr Gly Asp Gly Ala Leu Glu Asp Ala Arg	
145 150 155 160	
CGT CTG CGG GAG GGC AAC TGG GCA TGA GTG AGC ACA GTG GTG ACG GGG	528
Arg Leu Arg Glu Gly Asn Trp Ala Val Ser Thr Val Val Thr Gly	
165 170 175	
GCC GTG GCA CTG GGG GCC CTG GTA ACT GTA GGG GCC TTT TTT GCT AGC	576
Ala Val Ala Leu Gly Ala Leu Val Thr Val Gly Ala Phe Phe Ala Ser	
180 185 190	
AAG TG	582
Lys	

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(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 193 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met	Pro	Thr	Pro	Ala <sub>5</sub>	Ser	Thr	Pro	Asp	Thr <sub>10</sub>	Arg	Ala	Leu	Val	Ala	Asp 15
Phe	Val	Gly	Tyr <sub>20</sub>	Arg	Leu	Arg	Gln	Lys <sub>25</sub>	Gly	Tyr	Val	Cys	Gly <sub>30</sub>	Ala	Gly
Pro	Gly	Glu	Gly	Pro	Ala	Ala	Asp <sub>40</sub>	Pro	Leu	His	Gln	Ala <sub>45</sub>	Met	Arg	Ala
Ala	Gly <sub>50</sub>	Asp	Glu	Phe	Glu	Thr <sub>55</sub>	Arg	Phe	Arg	Arg	Thr <sub>60</sub>	Phe	Ser	Asp	Leu
Ala	Ala	Gln	Leu	His	Val <sub>70</sub>	Thr	Pro	Gly	Ser	Ala <sub>75</sub>	Gln	Gln	Arg	Phe	Thr <sub>80</sub>
Gln	Val	Ser	Asp	Glu <sub>85</sub>	Leu	Phe	Gln	Gly	Gly <sub>90</sub>	Pro	Asn	Trp	Gly	Arg <sub>95</sub>	Leu
Val	Ala	Phe	Phe <sub>100</sub>	Val	Phe	Gly	Ala	Ala <sub>105</sub>	Leu	Cys	Ala	Glu	Ser	Val	Asn
Lys	Glu	Met <sub>115</sub>	Glu	Pro	Leu	Val	Gly <sub>120</sub>	Gln	Val	Gln	Asp	Trp <sub>125</sub>	Ile	Val	Ala
Tyr	Leu	Glu	Thr	Arg	Leu	Ala <sub>135</sub>	Asp	Trp	Ile	His	Ser <sub>140</sub>	Ser	Gly	Gly	Trp
Ala	Asp	Phe	Thr	Ala	Leu <sub>150</sub>	Tyr	Gly	Asp	Gly	Ala <sub>155</sub>	Leu	Glu	Asp	Ala	Arg <sub>160</sub>
Arg	Leu	Arg	Glu	Gly <sub>165</sub>	Asn	Trp	Ala	*	Val <sub>170</sub>	Ser	Thr	Val	Val	Thr <sub>175</sub>	Gly
Ala	Val	Ala	Leu	Gly	Ala	Leu	Val	Thr <sub>185</sub>	Val	Gly	Ala	Phe	Phe	Ala	Ser <sub>190</sub>
Lys															